

10/587372

IAP11 Rec'd PCT/PTO 26 JUL 2006

SEQUENCE LISTING

<110> PUBLIC UNIVERSITY OF NAVARRA
<120> "Method of production of recombinant sucrose
5 synthase, use thereof in the manufacture of kits for determination of sucrose, production of ADPglucose and production of transgenic plants whose leaves and storage organs accumulate high contents of ADPglucose and starch".
10 <130> PCT-180
<150> ES 200400257
<151> 05.02.04
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15 <211> 25
<212> DNA
<213> *Solanum tuberosum*
<220>
<223> Promoter of the 5' region of *SS4*
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ctgccatggc tgaacgtgtt ttgac 25

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<223> Promoter of the 3' region of *SS4*
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<210> 3
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<223> *SSX*

<400>

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aaa cct cat gag ctt ttg gct gag ttc gat gca att cgc caa	168
gat gac aaa aac aaa ctg aac gaa cat gca ttc gaa gaa ctc	210
ctg aaa tcc act cag gaa gcg att gtt ctg ccc cct tgg gtt	252
gca ctt gct att cgt ttg agg cct ggt gtc tgg gaa tac atc	294
cgt gtg aac gtc aat gca cta gtt gtc gag gag ctg tcc gtc	336
cct gag tat ttg caa ttc aag gaa gaa ctt gtc gac gga gcc	378
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act gca tcc ttt cct aaa cca acc ctc acc aaa tct att gga	462
aat gga gtt gaa ttc ctc aat agg cac ctc tct gcc aaa atg	504
ttc cat gac aag gaa agc atg acc ccg ctt ctc gaa ttt ctt	546
cgc gct cac cat tat aag ggc aag aca atg atg ctg aat gat	588
agg ata cag aat tcg aat act ctt caa aat gtc cta agg aag	630
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gag aag ttc ttg ggg aga att cct atg gtt ttc aat gtg gtt	840
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gaa att gat gag ctg ctg tat agt gat gtt gag aat gac gag 1680
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 att gct gac act aag gga gct ttc gtt cag cct gca ttc tac 2016
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 tgc aag aaa gag cct tca cat tgg gaa acc att tcg acg ggt 2226
 ggc ctg aag cgc atc caa gag aag tac act tgg caa atc tac 2268
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 aaa cat gtt tct aaa ctt gat cgt cta gaa atc cgt cgc tat 2352
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 gct gtt cca ttg gct gct gag tga 2418

<210> 4

<211> 841

<212> protein

5 <213> *Solanum tuberosum*

<223> SSX fused with a histidine-rich amino acid tail deducted after expression of SSX in the pET-28a(+) expression plasmid

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val	leu	thr	arg	val	his	ser	leu	arg	glu	arg	val	asp	ala	thr	leu	ala	ala	his	arg				
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asn	glu	ile	leu	leu	phe	leu	ser	arg	ile	glu	ser	his	gly	lys	gly	ile	leu	lys	pro				
														65		70		75		80			
his	glu	leu	leu	ala	glu	phe	asp	ala	ile	arg	gln	asp	asp	lys	asn	lys	leu	asn	glu				
														85		90		95		100			
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 pro lys pro thr leu thr lys ser ile gly asn gly val glu phe leu asn arg his leu
 185 190 195 200
 ser ala lys met phe his asp lys glu ser met thr pro leu leu glu phe leu arg ala
 205 210 215 220
 his his tyr lys gly lys thr met met leu asn asp arg ile gln asn ser asn thr leu
 225 230 235 240
 gln asn val leu arg lys ala glu glu tyr leu ile met leu ser pro asp thr pro tyr
 245 250 255 260
 phe glu phe glu his lys phe gln glu ile gly leu glu lys gly trp gly asp thr ala
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 glu arg val leu glu met val cys met leu leu asp leu leu glu ala pro asp ser cys
 285 290 295 300
 thr leu glu lys phe leu gly arg ile pro met val phe asn val val ile leu ser pro
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 his gly tyr phe ala gln glu asn val leu gly tyr pro asp thr gly gly gln val val
 325 330 335 340
 tyr ile leu asp gln val pro ala leu glu arg glu met leu lys arg ile lys glu gln
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 gly leu asp ile ile pro arg ile leu ile val thr arg leu leu pro asp ala val gly
 365 370 375 380
 thr thr cys gly gln arg ile glu lys val tyr gly ala glu his ser his ile leu arg
 385 390 395 400
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 405 410 415 420
 pro tyr met glu thr phe ile glu asp val ala lys glu ile ser ala glu leu gln ala
 425 430 435 440
 lys pro asp leu ile ile gly asn tyr ser glu gly asn leu ala ala ser leu leu ala
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 his lys leu gly val thr gln cys thr ile ala his ala leu glu lys thr lys tyr pro
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 485 490 495 500
 ala asp leu ile ala met asn his thr asp phe ile ile thr ser thr phe gln glu ile
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 525 530 535 540
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 565 570 575 580
 his pro glu ile asp glu leu leu tyr ser asp val glu asn asp glu his leu cys val
 585 590 595 600
 leu lys asp arg thr lys pro ile leu phe thr met ala arg leu asp arg val lys asn
 605 610 615 620
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 625 630 635 640
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lys lys met tyr glu leu ile glu thr his asn leu asn gly gln phe arg trp ile ser
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 ser gln met asn arg val arg asn gly glu leu tyr arg tyr ile ala asp thr lys gly
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 cys gly leu pro thr phe ala thr asn his gly gly pro ala glu ile ile val his gly
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 lys ser gly phe his ile asp pro tyr his gly glu gln ala ala asp leu leu ala asp
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<210> 5

<211> 41

5 <212> DNA

<213> *Solanum tuberosum*

<220>

<223> "Forward" promoter required for the point mutagenesis of *SSX*.

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<400>

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<213> *Solanum tuberosum*

<220>

<223> "Reverse" promoter required for the point mutagenesis of *SSX*.

<400>

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5 <223> "Forward" promoter required for point mutagenesis
of *SSX*.

<400>
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<223> "Reverse" promoter required for the point
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25 <213> *Solanum tuberosum*
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of *SSX* and production of *SS5*.

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<220>

<223> "Reverse" promoter required for point mutagenesis
of *SSX* and production of *SS5*.

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10 <211> 2418

<212> DNA

<213> *Solanum tuberosum*

<220>

<223> *SS5*

15

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ctg	ttt	ctt	tca	agg	atc	gaa	agc	cac	gga	aaa	ggg	ata	ttg	126
aaa	cct	cac	gag	ctt	ttg	gct	gag	ttc	gat	gca	att	cgc	caa	168
gat	gac	aaa	aac	aaa	ctg	aac	gaa	cat	gca	ttc	gaa	gaa	ccc	210
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cgc	gct	cac	cat	tat	aag	ggc	aag	aca	atg	atg	ctg	aat	gat	588
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ggt	tat	ccc	gac	acc	ggt	ggc	cag	gtt	gtc	tac	att	tta	gat	924
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aca atg gca agg ttg gat cgt gtg aag aat tta act gga ctt 1764
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ctt gaa atg ttt tat gct ctc aag tac cgt aag atg gct gaa 2394
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<210> 12

5 <211> 841

<212> protein

<213> *Solanum tuberosum*

<223> SS5 fused with a histidine-rich amino acid sequence

<400>

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 545 550 555 560
 gly ala asp ile asn leu tyr phe ser tyr ser glu thr glu lys arg leu thr ala ser
 565 570 575 580
 his pro glu ile asp glu leu leu tyr ser asp val glu asn asp glu his leu cys val
 585 590 595 600
 leu lys asp arg thr lys pro ile leu phe thr met ala arg leu asp arg val lys asn
 605 610 615 620
 leu thr gly leu val glu trp tyr ala lys asn pro arg leu arg gly leu val asn leu
 625 630 635 640
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 cys gly leu pro thr phe ala thr asn his gly gly pro ala glu ile ile val his gly
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 745 750 755 760
 phe phe glu lys cys lys arg glu pro ser his trp glu thr ile ser thr asp gly leu
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 lys arg ile gln glu lys tyr thr trp gln ile tyr ser glu arg leu leu thr leu ala
 785 790 795 800
 ala val tyr gly phe trp lys his val ser lys leu asp arg leu glu ile arg arg tyr
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 825 830 835 840
 glu
 841